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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/813,323ADATE: 12/16/97
TIME: 15:28:36

INPUT SET: S22098.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Baltimore, David
6 Cheng, Genhong
7 Cleary, Aileen
8 Lederman, Seth
9 Ye, Zheng-sheng
10
11 (ii) TITLE OF INVENTION: TRUNCATED CRAF1 INHIBITS CD40 SIGNALING
12
13 (iii) NUMBER OF SEQUENCES: 5
14
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: Cooper & Dunham, LLP
17 (B) STREET: 1185 Avenue of the Americas
18 (C) CITY: New York
19 (D) STATE: New York
20 (E) COUNTRY: USA
21 (F) ZIP: 10036
22
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28
29 (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER:
31 (B) FILING DATE:
32 (C) CLASSIFICATION:
33
34 (viii) ATTORNEY/AGENT INFORMATION:
35 (A) NAME: White, John P
36 (B) REGISTRATION NUMBER: 28,678
37 (C) REFERENCE/DOCKET NUMBER: 50659
38
39 (ix) TELECOMMUNICATION INFORMATION:
40 (A) TELEPHONE: (212) 278-0400
41 (B) TELEFAX: (212) 391-0525
42
43
44 (2) INFORMATION FOR SEQ ID NO:1:
45
46 (i) SEQUENCE CHARACTERISTICS:

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47 (A) LENGTH: 566 amino acids
48 (B) TYPE: amino acid
49 (C) STRANDEDNESS: single
50 (D) TOPOLOGY: linear
51
52 (ii) MOLECULE TYPE: peptide
53
54
55 (ix) FEATURE:
56 (A) NAME/KEY: Peptide
57 (B) LOCATION: 1..566
58
59
60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
61
62 Met Glu Ser Ser Lys Lys Met Asp Ala Ala Gly Thr Leu Gln Pro Asn
63 1 5 10 15
64
65 Pro Pro Leu Lys Leu Gln Pro Asp Arg Gly Ala Gly Ser Val Leu Val
66 20 25 30
67
68 Pro Glu Gln Gly Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu Asp
69 35 40 45
70
71 Lys Tyr Lys Cys Glu Lys Cys Arg Leu Val Leu Cys Asn Pro Lys Gln
72 50 55 60
73
74 Thr Glu Cys Gly His Arg Phe Cys Glu Ser Cys Met Ala Ala Leu Leu
75 65 70 75 80
76
77 Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Ile Lys
78 85 90 95
79
80 Asp Lys Val Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala Leu
81 100 105 110
82
83 Gln Val Tyr Cys Arg Asn Glu Gly Arg Gly Cys Ala Glu Gln Leu Thr
84 115 120 125
85
86 Leu Gly His Leu Leu Val His Leu Lys Asn Glu Cys Gln Phe Glu Glu
87 130 135 140
88
89 Leu Pro Cys Leu Arg Ala Asp Cys Lys Glu Lys Val Leu Arg Lys Asp
90 145 150 155 160
91
92 Leu Arg Asp His Val Glu Lys Ala Cys Lys Tyr Arg Glu Ala Thr Cys
93 165 170 175
94
95 Ser His Cys Lys Ser Gln Val Pro Met Ile Lys Leu Gln Lys His Glu
96 180 185 190
97
98 Asp Thr Asp Cys Pro Cys Val Val Val Ser Cys Pro His Lys Cys Ser
99 195 200 205

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100
101      Val Gln Thr Leu Leu Arg Ser Glu Leu Ser Ala His Leu Ser Glu Cys
102          210                      215                      220
103
104      Val Asn Ala Pro Ser Thr Cys Ser Phe Lys Arg Tyr Gly Cys Val Phe
105          225                      230                      235                      240
106
107      Gln Gly Thr Asn Gln Gln Ile Lys Ala His Glu Ala Ser Ser Ala Val
108                      245                      250                      255
109
110      Gln His Val Asn Leu Leu Lys Glu Trp Ser Asn Ser Leu Glu Lys Lys
111                      260                      265                      270
112
113      Val Ser Leu Leu Gln Asn Glu Ser Val Glu Lys Asn Lys Ser Ile Gln
114                      275                      280                      285
115
116      Ser Leu His Asn Gln Ile Cys Ser Phe Glu Ile Glu Ile Glu Arg Gln
117          290                      295                      300
118
119      Lys Glu Met Leu Arg Asn Asn Glu Ser Lys Ile Leu His Leu Gln Arg
120          305                      310                      315                      320
121
122      Val Ile Asp Ser Gln Ala Glu Lys Leu Lys Glu Leu Asp Lys Glu Ile
123                      325                      330                      335
124
125      Arg Pro Phe Arg Gln Asn Trp Glu Glu Ala Asp Ser Met Lys Ser Ser
126                      340                      345                      350
127
128      Val Glu Ser Leu Gln Asn Arg Val Thr Glu Leu Glu Ser Val Asp Lys
129          355                      360                      365
130
131      Ser Ala Gly Gln Ala Ala Arg Asn Thr Gly Leu Leu Glu Ser Gln Leu
132          370                      375                      380
133
134      Ser Arg His Asp Gln Thr Leu Ser Val His Asp Ile Arg Leu Ala Asp
135          385                      390                      395                      400
136
137      Met Asp Leu Arg Phe Gln Val Leu Glu Thr Ala Ser Tyr Asn Gly Val
138                      405                      410                      415
139
140      Leu Ile Trp Lys Ile Arg Asp Tyr Lys Arg Arg Lys Gln Glu Ala Val
141                      420                      425                      430
142
143      Met Gly Lys Thr Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr Gly Tyr
144          435                      440                      445
145
146      Phe Gly Tyr Lys Met Cys Ala Arg Val Tyr Leu Asn Gly Asp Gly Met
147          450                      455                      460
148
149      Gly Lys Gly Thr His Leu Ser Leu Phe Phe Val Ile Met Arg Gly Glu
150          465                      470                      475                      480
151
152      Tyr Asp Ala Leu Leu Pro Trp Pro Phe Lys Gln Lys Val Thr Leu Met

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	485	490	495
153			
154			
155	Leu Met Asp Gln Gly Ser Ser Arg Arg His Leu Gly Asp Ala Phe Lys		
156	500	505	510
157			
158	Pro Asp Pro Asn Ser Ser Ser Phe Lys Lys Pro Thr Gly Glu Met Asn		
159	515	520	525
160			
161	Ile Ala Ser Gly Cys Pro Val Phe Val Ala Gln Thr Val Leu Glu Asn		
162	530	535	540
163			
164	Gly Thr Tyr Ile Lys Asp Asp Thr Ile Phe Ile Lys Val Ile Val Asp		
165	545	550	555
166			560
167	Thr Ser Asp Leu Pro Asp		
168	565		
169			

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

188	Met Glu Ser Ser Lys Lys Met Asp Ser Pro Gly Ala Leu Gln Thr Asn
189	1 5 10 15
191	Pro Pro Leu Lys Leu His Thr Asp Arg Ser Ala Gly Thr Pro Val Phe
192	20 25 30
193	
194	Val Pro Glu Gln Gly Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu
195	35 40 45
196	
197	Asp Lys Tyr Lys Cys Glu Lys Cys His Leu Val Leu Cys Ser Pro Lys
198	50 55 60
199	
200	Gln Thr Glu Cys Gly His Arg Phe Cys Glu Ser Cys Met Ala Ala Leu
201	65 70 75 80
202	
203	Leu Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Val
204	85 90 95
205	

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206	Lys Asp Lys Val Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile L u Ala
207	100 105 110
208	
209	Leu Gln Ile Tyr Cys Arg Asn Glu Ser Arg Gly Cys Ala Glu Gln Leu
210	115 120 125
211	
212	Thr Leu Gly His Leu Leu Val His Leu Lys Asn Asp Cys His Phe Glu
213	130 135 140
214	
215	Glu Leu Pro Cys Val Arg Pro Asp Cys Lys Glu Lys Val Leu Arg Lys
216	145 150 155 160
217	
218	Asp Leu Arg Asp His Val Glu Lys Ala Cys Lys Tyr Arg Glu Ala Thr
219	165 170 175
220	
221	Cys Ser His Cys Lys Ser Gln Val Pro Met Ile Ala Leu Gln Lys His
222	180 185 190
223	
224	Glu Asp Thr Asp Cys Pro Cys Val Val Val Ser Cys Pro His Lys Cys
225	195 200 205
226	
227	Ser Val Gln Thr Leu Leu Arg Ser Glu Leu Ser Ala His Leu Ser Glu
228	210 215 220
229	
230	Cys Val Asn Ala Pro Ser Thr Cys Ser Phe Lys Arg Tyr Gly Cys Val
231	225 230 235 240
232	
233	Phe Gln Gly Thr Asn Gln Gln Ile Lys Ala His Glu Ala Ser Ser Ala
234	245 250 255
235	
236	Val Gln His Val Asn Leu Leu Lys Glu Trp Ser Asn Ser Leu Glu Lys
237	260 265 270
238	
239	Lys Val Ser Leu Leu Gln Asn Glu Ser Val Glu Lys Asn Lys Ser Ile
240	275 280 285
241	
242	Gln Ser Leu His Asn Gln Ile Cys Ser Phe Glu Ile Glu Ile Glu Arg
243	290 295 300
244	
245	Gln Lys Glu Met Leu Arg Asn Asn Glu Ser Lys Ile Leu His Leu Gln
246	305 310 315 320
247	
248	Arg Val Ile Asp Ser Gln Ala Glu Lys Leu Lys Glu Leu Asp Lys Glu
249	325 330 335
250	
251	Ile Arg Pro Phe Arg Gln Asn Trp Glu Glu Ala Asp Ser Met Lys Ser
252	340 345 350
253	
254	Ser Val Glu Ser Leu Gln Asn Arg Val Thr Glu Leu Glu Ser Val Asp
255	355 360 365
256	
257	Lys Ser Ala Gly Gln Val Ala Arg Asn Thr Gly Leu Leu Glu Ser Gln
258	370 375 380

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SEQUENCE VERIFICATION REPORT
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Error

Original Text